

FIG. 1A

11 20 29 38 47 56
 5' GAG ACT CAC GGT CAA GCT AAG GCG AAG AGT GGG TGG CTG AAG CCA TAC TAT TTT

 65 74 83 92 101 110
 ATA GAA TTA ATG GAA AGC AGA AAA GAC ATC ACA AAC CAA GAA GAA CTT TGG AAA

 M E S R K D I T N Q E E L W K

 119 128 137 146 155 164
 ATG AAG CCT AGG AGA AAT TTA GAA GAA GAC GAT TAT TTG CAT AAG GAC ACG GGA

 M K P R R N L E E D D Y L H K D T G

 173 182 191 200 209 218
 GAG ACC AGC ATG CTA AAA AGA CCT GTG CTT TTG CAT TTG CAC CAA ACA GCC CAT

 E T S M L K R P V L L H L H Q T A H

 227 236 245 254 263 272
 GCT GAT GAA TTT GAC TGC CCT TCA GAA CTT CAG CAC ACA CAG GAA CTC TTT CCA

 A D E F D C P S E L Q H T Q E L F P

 281 290 299 308 317 326
 CAG TGG CAC TTG CCA ATT AAA ATA GCT GCT ATT ATA GCA TCT CTG ACT TTT CTT

 Q W H L P I K I A A I I A S L T F L

 335 344 353 362 371 380
 TAC ACT CTT CTG AGG GAA GTA ATT CAC CCT TTA GCA ACT TCC CAT CAA CAA TAT

 Y T L L R E V I H P L A T S H Q Q Y

 389 398 407 416 425 434
 TTT TAT AAA ATT CCA ATC CTG GTC ATC AAC AAA GTC TTG CCA ATG GTT TCC ATC

 F Y K I P I L V I N K V L P M V S I

 443 452 461 470 479 488
 ACT CTC TTG GCA TTG GTT TAC CTG CCA GGT GTG ATA GCA GCA ATT GTC CAA CTT

 T L L A L V Y L P G V I A A I V Q L

 497 506 515 524 533 542
 CAT AAT GGA ACC AAG TAT AAG AAG TTT CCA CAT TTG TTG GAT AAG TGG ATG TTA

 H N G T K Y K K F P H W L D K W M L

 551 560 569 578 587 596
 ACA AGA AAG CAG TTT GGG CTT CTC AGT TTC TTT TTT GCT GTA CTG CAT GCA ATT

 T R K Q F G L L S F F F A V L H A I

 605 614 623 632 641 650
 TAT AGT CTG TCT TAC CCA ATG AGG CGA TCC TAC AGA TAC AAG TTG CTA AAC TGG

 Y S L S Y P M R R S Y R Y K L L N W

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659 668 677 686 695 704
 GCA TAT CAA CAG GTC CAA CAA AAT AAA GAA GAT GCC TGG ATT GAG CAT GAT GTT
 A Y Q Q V Q Q N K E D A W I E H D V
 713 722 731 740 749 758
 TGG AGA ATG GAG ATT TAT GTG TCT CTG GGA ATT GTG GGA TTG GCA ATA CTG GCT
 W R M E I Y V S L G I V G L A I L A
 767 776 785 794 803 812
 CTG TTG GCT GTG ACA TCT ATT CCA TCT GTG AGT GAC TCT TTG ACA TGG AGA GAA
 L L A V T S I P S V S D S L T W R E
 821 830 839 848 857 866
 TTT CAC TAT ATT CAG AGC AAG CTA GGA ATT GTT TCC CTT CTA CTG GGC ACA ATA
 F H Y I Q S K L G I V S L L L G T I
 875 884 893 902 911 920
 CAC GCA TTG ATT TTT GCC TGG AAT AAG TGG ATA GAT ATA AAA CAA TTT GTA TGG
 H A L I F A W N K W I D I K Q F V W
 929 938 947 956 965 974
 TAT ACA CCT CCA ACT TTT ATG ATA GCT GTT TTC CTT CCA ATT GTT GTC CTG ATA
 Y T P P T F M I A V F L P I V V L I
 983 992 1001 1010 1019 1028
 TTT AAA AGC ATA CTA TTC CTG CCA TGC TTG AGG AAG AAG ATA CTG AAG ATT AGA
 F K S I L F L P C L R K K I L K I R
 1037 1046 1055 1064 1073 1082
 CAT GGT TGG GAA GAC GTC ACC AAA ATT AAC AAA ACT GAG ATA TGT TCC CAG TTG
 H G W E D V T K I N K T E I C S Q L
 1091 1100 1109 1118 1127 1136
 TAG AAT TAC TGT TTA CAC ACA TTT TTG TTC AAT ATT GAT ATA TTT TAT CAC CAA
 * N Y C L H T F L F N I D I F Y H Q
 1145 1154 1163 1172 1181 1190
 CAT TTC AAG TTT GTA TTT GTT AAT AAA ATG ATT ATT CAA GGA AAA AAA AAA AAA
 H F K F V F V N K M I I Q G K K K K

AAA AA 3'

K

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FIG. 1B

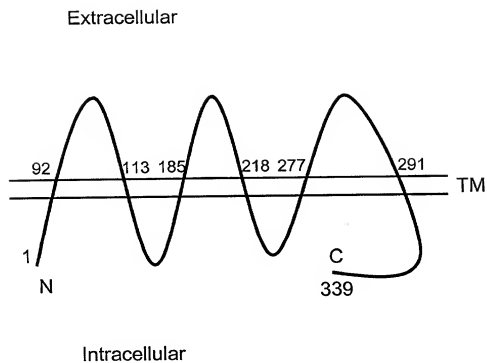
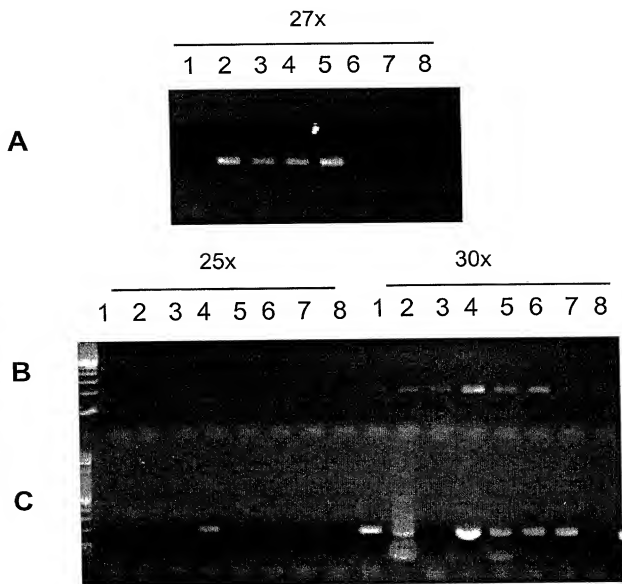


FIG. 1C

5' GGC GGA GGC GGA GGC GGA GGG CGA GGG GCG GGG AGC GCC GCC TGG AGC GCG
GCA GGT CAT ATT GAA CAT TCC AGA TAC CTA TCA TTA CTC GAT GCT GTT GAT
AAC AGC AAG 3'

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FIG. 2



Panels:

A

1. Brain
2. Prostate
3. LAPC-4 AD
4. LAPC-4 AI
5. LAPC-9 AD
6. HeLa
7. Murine cDNA
8. Neg. control

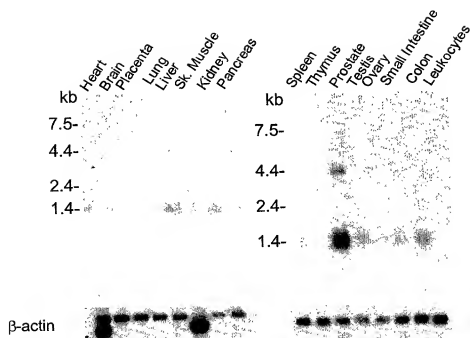
B

1. Brain
2. Heart
3. Kidney
4. Liver
5. Lung
6. Pancreas
7. Placenta
8. Skeletal Muscle

C

1. Colon
2. Ovary
3. Leukocytes
4. Prostate
5. Small Intestine
6. Spleen
7. Testis
8. Thymus

FIG. 3A



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FIG. 3B

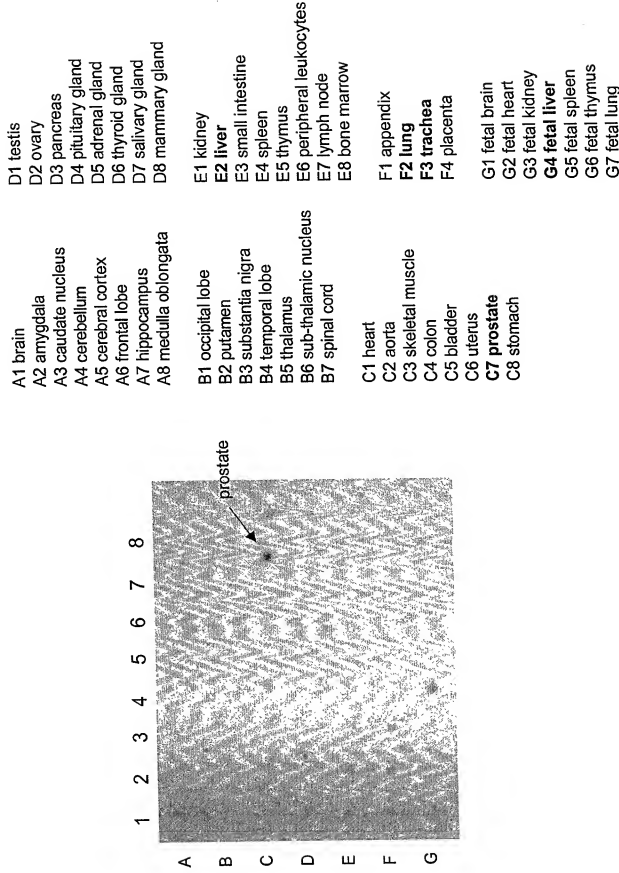


FIG. 4

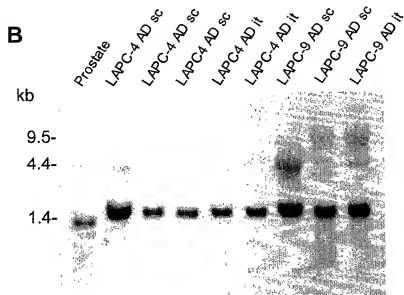
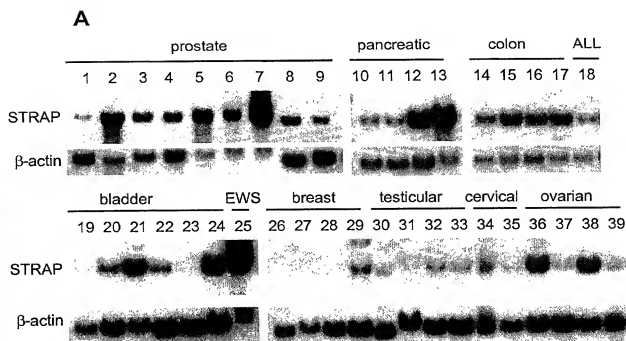
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 CGCAACTATCCCTTCTACATGTCCACACGTATACTCCAACACTTTATTAGGCATCTGATTAGTTTGGAAAGTATGC
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FIG. 5



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FIG. 6

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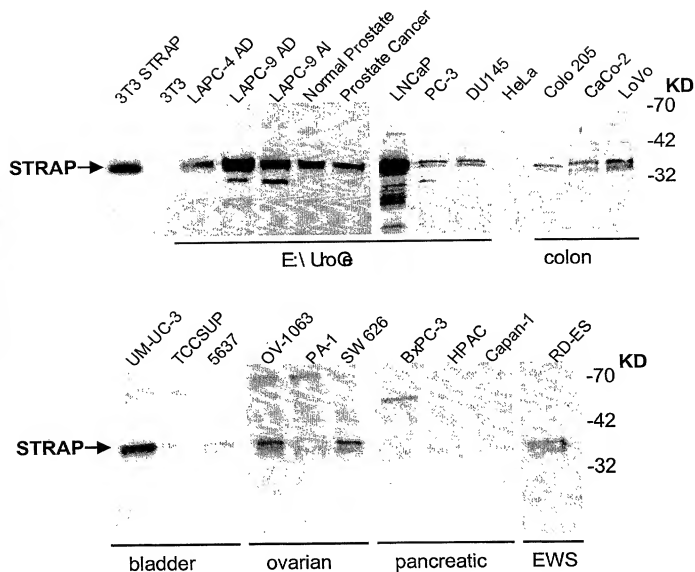
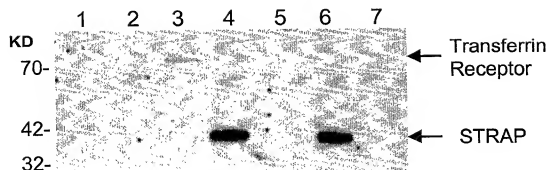
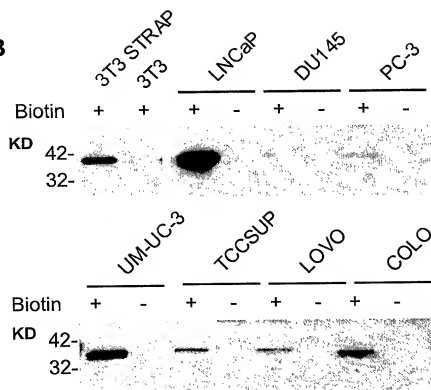


FIG. 7

A

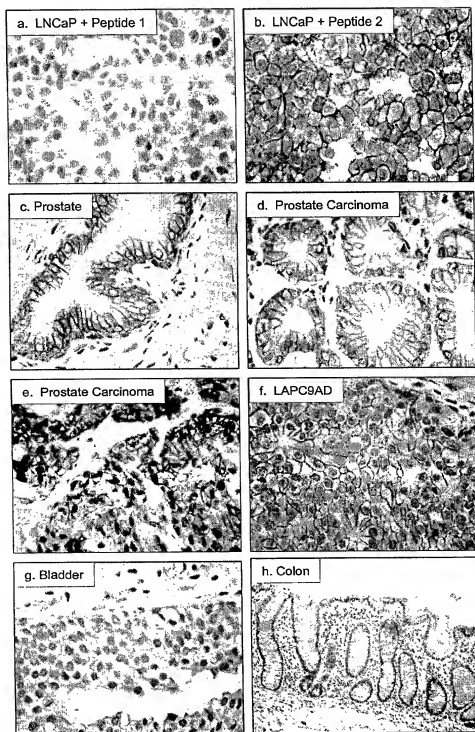


B



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FIG. 8



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FIG. 9

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5'   10       19       28       37       46       55
    GAC TTT TAC AAA ATT CCT ATA GAG ATT GTG AAT AAA ACC TTA CCT ATA GTT GCC
    --- --- --- --- --- --- --- --- --- --- --- --- ---
    Asp Phe Tyr Lys Ile Pro Ile Glu Ile Val Asn Lys Thr Leu Pro Ile Val Ala

       64       73       82       91      100      109
    ATT ACT TTG CTC TCC CTA GTA TAC CTC GCA GGT CTT CTG GCA GCT GCT TAT CAA
    --- --- --- --- --- --- --- --- --- --- --- --- ---
    Ile Thr Leu Leu Ser Leu Val Tyr Leu Ala Gly Leu Leu Ala Ala Ala Tyr Gln

      118      127      136      145      154      163
    CTT TAT TAC GGC ACC AAG TAT AGG AGA TTT CCA CCT TGG TTG GAA ACC TGG TTA
    --- --- --- --- --- --- --- --- --- --- --- --- ---
    Leu Tyr Tyr Gly Thr Lys Tyr Arg Arg Phe Pro Pro Trp Leu Glu Thr Trp Leu

      172      181      190      199      208      217
    CAG TGT AGA AAA CAG CTT GGA TTA CTA AGT TTT TTC TTC GCT ATG GTC CAT GTT
    --- --- --- --- --- --- --- --- --- --- --- --- ---
    Gln Cys Arg Lys Gln Leu Gly Leu Leu Ser Phe Phe Phe Ala Met Val His Val

      226      235      244      253      262      271
    GCC TAC AGC CTC TGC TTA CCG ATG AGA AGG TCA GAG AGA TAT TTG TTT CTC AAC
    --- --- --- --- --- --- --- --- --- --- --- --- ---
    Ala Tyr Ser Leu Cys Leu Pro Met Arg Arg Ser Glu Arg Tyr Leu Phe Leu Asn

      280      289      298      307      316      325
    ATG GCT TAT CAG CAG GTT CAT GCA AAT ATT GAA AAC TCT TGG AAT GAG GAA GAA
    --- --- --- --- --- --- --- --- --- --- --- --- ---
    Met Ala Tyr Gln Gln Val His Ala Asn Ile Glu Asn Ser Trp Asn Glu Glu Glu

      334      343      352      361      370      379
    GTT TGG AGA ATT GAA ATG TAT ATC TCC TTT GGC ATA ATG AGC CTT GGC TTA CTT
    --- --- --- --- --- --- --- --- --- --- --- --- ---
    Val Trp Arg Ile Glu Met Tyr Ile Ser Phe Gly Ile Met Ser Leu Gly Leu Leu

      388      397      406      415      424      433
    TCC CTC CTG GCA GTC ACT TCT ATC CCT TCA GTG AGC AAT GCT TTA AAC TGG AGA
    --- --- --- --- --- --- --- --- --- --- --- --- ---
    Ser Leu Leu Ala Val Thr Ser Ile Pro Ser Val Ser Asn Ala Leu Asn Trp Arg

      442      451      460      469      478      487
    GAA TTC AGT TTT ATT CAG TCT ACA CTT GGA TAT GTC GCT CTG CTC ATA AGT ACT
    --- --- --- --- --- --- --- --- --- --- --- --- ---
    Glu Phe Ser Phe Ile Gln Ser Thr Leu Gly Tyr Val Ala Leu Leu Ile Ser Thr

      496      505      514
    TTC CAT GTT TTA ATT TAT GGA TGG AAA CGA GCT 3'
    --- --- --- --- --- --- --- --- --- --- --- --- ---
    Phe His Val Leu Ile Tyr Gly Trp Lys Arg Ala

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FIG. 10

STRAP-2, AA508880 (NCI CGAP Pr6)

ggctgacattttctttattccttctgtcagagatctgattcatccatatgctagaacccaacagagtgacttttaca
aaattcctatagagattgtgaataaaaaccttacctatagttgccattactttgctctccctagtataaccttgcagg
tcttctggcagctgcttaccactttattacggccaccaagtataggagatttccaccttgggtggaaacctgggtta
cagtgtagaaaaacagcttgattactaagttgtttcttcgctatgggtccatgttgctacagcctctgcttaccga
tgagaaggtcagagagat

STRAP-2, 98P4B6 SSH fragment

TTTGACGCTTTGCAGATACCCAGACTGAGCTGGAACCTGGAATTTGTCTTCTTATTGACTCTACTCTTTTAAAGCG
GCTGCCATTACATTCTCTCAGCTGTCTCTTGCACTTAGGTGTACATGTGACTGAGTGTGGCCAGTGAGATGAAGTC
TCCTCAAAGGAAGGCAGCATGTGTCTTTTT

AI139607 (testis EST)

aagaaggagaatccatttagcacctcctcagcctggctcagtgattcatatgtggctttgggaataacttgggtttt
tctgttgttactcttgggaatcacttctttgccatctgttagcaatgcagtcacttggagagattccgattttgt
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R80991 (placental EST)

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tgcttgcattcagccgnaga

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FIG. 11A

```

STRAP-1      106  FYKIPILVINKVLPMSITLLALVYLPGVIAAIVQLHNGTIKKKFPHWLDKQMLTRKQPG
STRAP-2      2   FYKIPIEIVNKTLPVAILLLSLVYLAGLLAAAYQLYYGTKYRRFPNWLETWLQCRKQLG
                *****  * * * * * * * * * * * * * * * * * * * * * * * * * * * *

STRAP-1     166  LLSFFFFAVLHAIYSLSYPMRRSRYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEIYVSLGIV
STRAP-2     62  LLSFFFFAMVHVAYSLCLPMRRSERYLFLNMAYQQVHANIEWSWNEEEVWRIEMYISPGIM
                *****  * * * * * * * * * * * * * * * * * * * * * * * * * * * *

STRAP-1     226  GLAILALLAVTSIPSVSDSLTWREFHYIQSKLGIVSLLGLTIHALIFAWNK
STRAP-2    122  SLGLLSLLAVTSIPSVSNALNWRREFSFIQSTLGYVALLISTFHVLIYGNKR
                * * * * * * * * * * * * * * * * * * * * * * * * * * * *

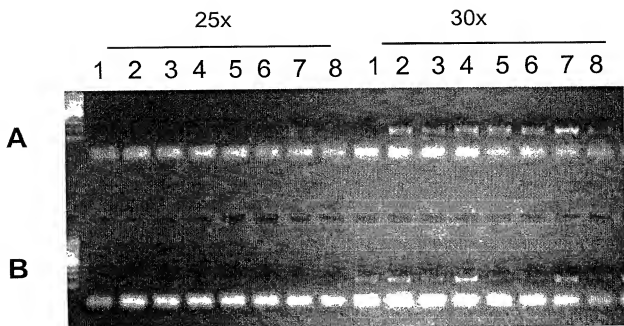
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FIG. 11B

	15	16	30	31	45	46	60	61	75	76	90
STRAP-1	MESKIDITNQBELWK	MKRRNLEEDYLLK	DTGETSNLAREVLLH	LHOTNADEFDCPE	LOHTQELFFOWHLPI	KIAAIASLITFLYTL					90
STRAP-2	-----	-----	-----	-----	-----	-----					0
STRAP-3	-----	-----	-----	-----	-----	-----					0
STRAP-4	-----	-----	-----	-----	-----	-----					0
	105	106	120	121	135	136	150	151	165	166	180
STRAP-1	LREVIHPLATSHQOY	FYKIPILVINKVLEW	VSITLDAVILPGVI	KALVQIHNGKTKKKE	PHWDDKMLTRKQCP	ELSTFFANVIAKSTL					180
STRAP-2	-----	-----	-----	-----	-----	-----					76
STRAP-3	-----	-----	-----	-----	-----	-----					0
STRAP-4	-----	-----	-----	-----	-----	-----					0
	195	196	210	211	225	226	240	241	255	256	270
STRAP-1	SPMRRNSRYKILNW	FYQVQONKEDAMIE	HDVWRMEIYVSGVI	GLAILANGAVTSIPS	NSDSLWREPHYLQS	KQIVSILMLKTHAL					270
STRAP-2	CLPMRRNSRYLFLNW	FYQOVHANISWNE	BEVWRLEMTISFQTH	SLGLLSPLANTTSIPS	VSNHLNWRPSTQS	NSGVALLASTVAVI					166
STRAP-3	-----	-----	-----	-----	-----	-----					68
STRAP-4	-----	-----	-----	-----	-----	-----					82
	285	286	300	301	315	316	330	331	345	346	360
STRAP-1	IFANKKVIDIKQFVW	YIPTFTNLNPLPIV	VLEPKSILFLPCLPK	KILKIHGHEVDVTKI	NKTEICSQL						360
STRAP-2	YGNWCPA-----	-----	-----	-----	-----						173
STRAP-3	YVGGKRLSPSNLRW	YILPAATVGLITPCT	VTVILKFLVILMPCQDN	TUTRLKOOCHENSKH							128
STRAP-4	TYGWRAPFESRYKE	YIPTFTITVLLVPCV	RSSWAKALFLPCIQ	P-----	-----						128

FIG. 12

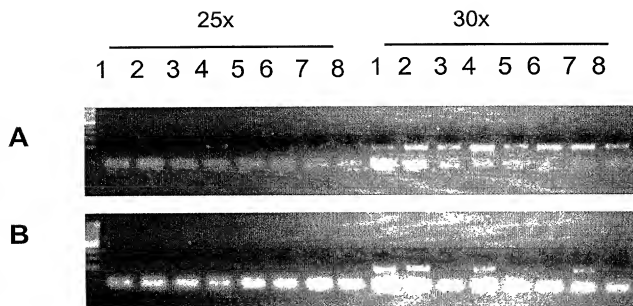


- A**
1. Brain
 2. Heart
 3. Kidney
 4. Liver
 5. Lung
 6. Pancreas
 7. Placenta
 8. Skeletal Muscle

- B**
1. Colon
 2. Ovary
 3. Leukocytes
 4. Prostate
 5. Small Intestine
 6. Spleen
 7. Testis
 8. Thymus

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FIG. 13



- A**
1. Brain
 2. Heart
 3. Kidney
 4. Liver
 5. Lung
 6. Pancreas
 7. Placenta
 8. Skeletal Muscle

- B**
1. Colon
 2. Ovary
 3. Leukocytes
 4. Prostate
 5. Small Intestine
 6. Spleen
 7. Testis
 8. Thymus

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FIG.14

26x

1 2 3 4 5 6 7 8

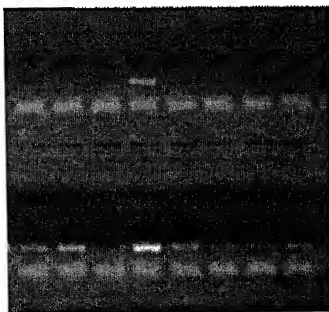
A



B

1 2 3 4 5 6 7 8

25x



30x

A

1. Brain
2. Prostate
3. LAPC-4 AD
4. LAPC-4 AI
5. LAPC-9 AD
6. HeLa
7. Murine cDNA
8. Neg. control

B

1. Colon
2. Ovary
3. Leukocytes
4. Prostate
5. Small Intestine
6. Spleen
7. Testis
8. Thymus

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FIG. 15

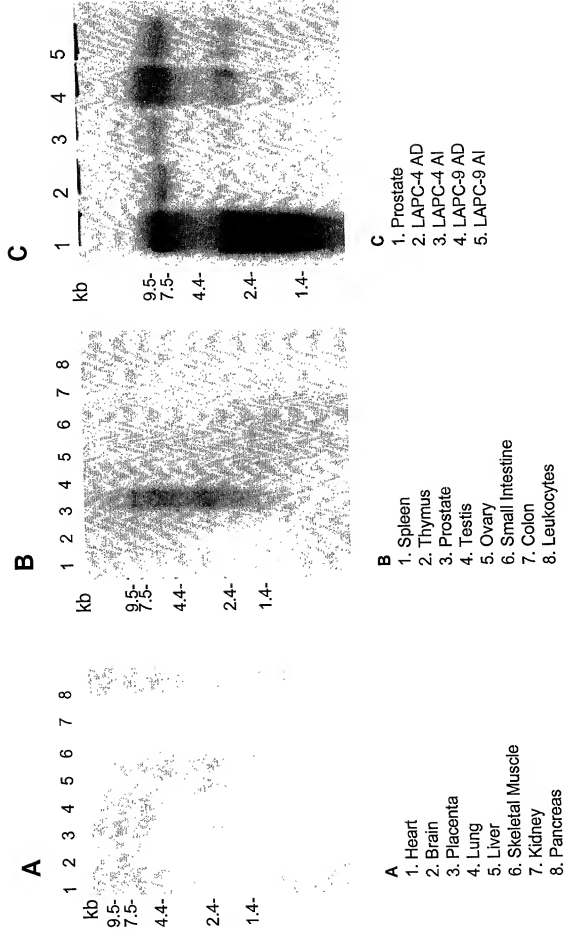
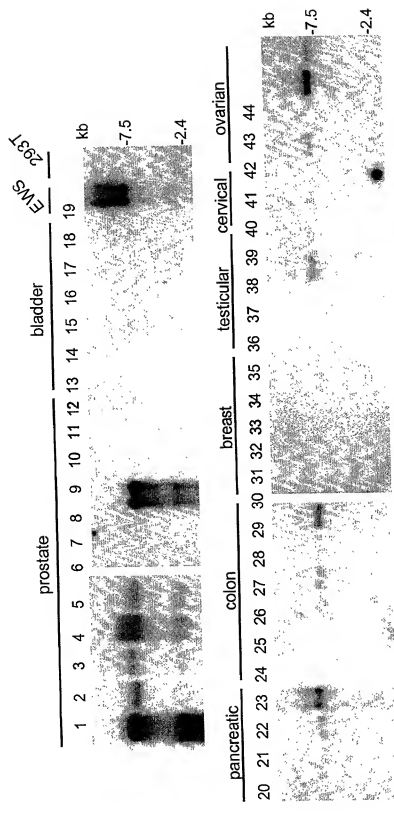


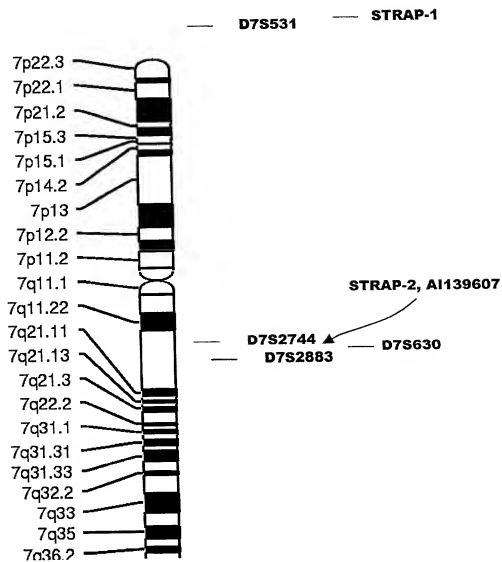
FIG. 16



- | | | |
|---------------|-----------------|-------------|
| 1. prostate | 20. PANC-1 | 39. A431 |
| 2. LAPC-4 AD | 21. BxPC-3 | 40. HeLa |
| 3. LAPC-4 AI | 22. HPAC | 41. OV-1063 |
| 4. LAPC-9 AD | 23. Capan-1 | 42. PA-1 |
| 5. LAPC-9 AI | 24. LS180 | 43. SW626 |
| 6. TsuP1 | 25. SK-CO-1 | 44. CAOV-3 |
| 7. DU145 | 26. CaCo-2 | |
| 8. LNCaP | 27. LoVo | |
| 9. PC-3 | 28. T84 | |
| 10. LAPC-4 CL | 29. Colo-205 | |
| 11. PrEC | | |
| | 30. BT-20 | |
| | 31. CAMA-1 | |
| | 32. DU4475 | |
| | 33. MCF-7 | |
| | 34. MDA-MB-435s | |
| | 35. NTERA-2 | |
| | 36. NCCIT | |
| | 37. TERA-1 | |
| | 38. TERA-2 | |

FIG. 17

GDB Comprehensive



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FIG. 18

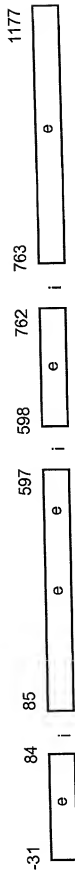
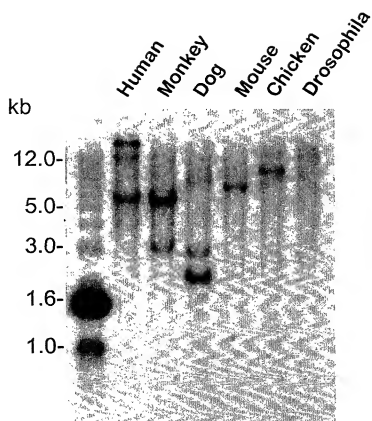
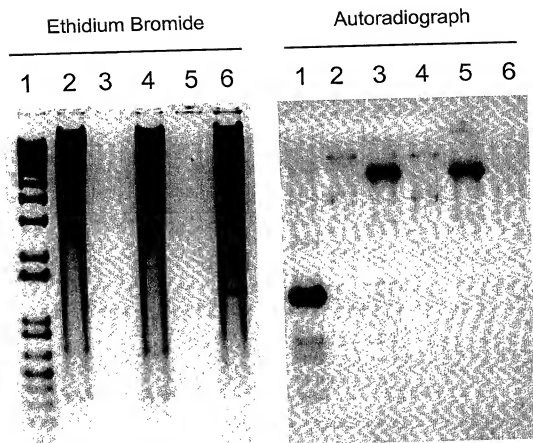


FIG. 19



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FIG. 20



Lanes

- 1) 1kb ladder
- 2) human female genomic
- 3) 12P11 BAC mus
- 4) human female genomic
- 5) 12P11 BAC mus
- 6) 3T3